

A number theoretical observation about the degeneracy of the genetic code

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Abstract

We discuss the similarity of the degeneration structure of the genetic code with a pure number theoretic – “divisors code.” The most interesting thing about our observation is not that there is a connection between number theory and the genetic code, but the simplicity of the rule. We hope that the observation and the naive model presented in this paper will serve for ideas to other models of the degeneracy of the genetic code. Maybe, the ideas of this article can also be used in the area of artificial life to synthesize artificial genetic codes.

1 Introduction

Recently there was shown a lot of interest to number theoretic studies of the problem of degeneration of the genetic code, see [1]– [5]. In this paper we emphasize the similarity of the degeneration structure of the genetic code and a so called “divisors code.” The latter one arises very naturally from purely number theoretic arguments.

2 Genetic code

The information contained in the DNA molecule is translated into aminoacids by the messenger and the transcription RNA. The aminoacids form protein molecules. A sequence of three nukleotides in the mRNA molecule, a so called codon, encodes for a specific aminoacid. However, there are different codons that encode for the same aminoacid. This degeneracy of the genetic code is still not fully understood. In this article we mean the so called standard genetic code when we talk about genetic code. We have used Wikipedia [6] to get information about the genetic code.

In this article it will be announce an unpredicted similarity between the degeneracy of the genetic code and the number of positive divisors of the first the first 20 integers. The idea that there are some similarities between the number theory and the genetic code is not new. In [1] the set of the first 18 prime numbers together with 0 och 1 is used for representing the aminoacids.

We also present a model (based on the observation) that simulates an artificial genetic code.

3 The number theoretic observation about the genetic code

Let A be the set of aminoacids. We let $A(k)$ denote the number of aminoacids in A that are encoded by k codons. If we use the standard genetic code we get the following table.

k	$A(k)$
1	2
2	9
3	1
4	5
5	0
6	3

Now, let $B = \{1, 2, \dots, 20\}$. The number of positive divisors of a positive integer m is denoted by $\tau(m)$. By $B(k)$ we mean the number of elements in B that have k positive divisors. Hence

$$B(k) = \{b \in B; \tau(b) = k\}.$$

Let us add $B(k)$, $1 \leq k \leq 6$ as a third column in the table above.

k	$A(k)$	$B(k)$
1	2	1
2	9	8
3	1	2
4	5	5
5	0	1
6	3	3

The match between the second and the third column is not absolut but it is still remarkable. We use this observation to construct an elementary “genetic code like model”, abbreviated GCLM, in the next section.

In the standard genetic code there are 3 codons, that do not encode for an aminoacid, they encode for that the end of the protein is reached. We say that these codes encode for STOP. If we add the STOP to the set of aminoacids and let $B = \{1, 2, \dots, 21\}$ we get the following table:

k	$A(k)$	$B(k)$
1	2	1
2	9	8
3	2	2
4	5	6
5	0	1
6	3	3

4 A number theoretical “genetic code”

The number of positive divisors of a positive integer m is the same as the number of pairs of the form (a, b) , where $a, b \geq 1$ and $a \cdot b = m$. This can be visualized as the number of rectangles with integer side lengths and area m that can be formed.

The idea is that the numbers $1, 2, \dots, 20$ represent 20 different aminoacids. The pairs of positive numbers of the form (a, b) , where $ab = m$, represents the codons that code for the aminoacid represented by m . We call such a code *divisors code*.

Of course, it is easy to generalize this to any number of aminoacids (building blocks).



Figure 4.1:

Example 4.1. The code sequence

$$((1, 3), (5, 2), (3, 1), (2, 1), (2, 3), (1, 4), (11, 1), (6, 3)) \quad (4.1)$$

encode for the sequence

$$(3, 10, 3, 2, 6, 4, 11, 18).$$

A possible visualization of the code sequence is shown in Figure 4.1.

Example 4.2. Let us consider a toy genetic model in that the alphabet has just two letters, say $A = 0$ and $B = 1$, codons have the length 3: AAA, AAB, \dots, BBB . There are totally 8 codons. We suppose that they should encode 4 aminoacids: $B = \{1, 2, 3, 4\}$. Aminoacids are encoded as follows: $1 = (1, 1)$, $2 = \{(1, 2), (2, 1)\}$, $3 = \{(3, 1), (1, 3)\}$, $4 = \{(1, 4), (4, 1), (2, 2)\}$. Here (in contrast to the standard genetic code) the total number of codons matches with the total number of divisors.

5 Discussion

The most interesting thing about our observation is not that there is a connection between number theory and the genetic code, but the simplicity of the rule.

We hope that the observation and the naive model presented in this paper will serve for ideas to other models of the degeneracy of the genetic code. Maybe, the ideas of this article can also be used in the area of artificial life to synthesize artificial genetic codes.

The divisors code which was presented in this article would match precisely with the genetic code if for any k the number $A(k)$ were equal to the number $B(k)$. We see that there are deviations. Hence, Nature did not follow precisely to the laws of number theory. There might happen some mutations which disturbed the genetic code.

Results of this note were announced in [7]

References

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